

Derivation of the code for amino acids

For the average proportions of amino acids (Cf. Atlas of protein sequence and structure, loc. cit.: Gly = 8,4%, Ala = 8,6%, Ser = 7,0%, Pro+Val+Thr+Cys = 20,8%, Leu+Ile+Asn+Asp = 21,7%, Gln+Lys+Glu+Met = 18,2%, His = 2,0%, Phe = 3,6%, Arg+Tyr = 8,3%, Trp = 1,3%), the global harmonic distance (computed over all the possible pairs of frequencies after synchronization, i. e. over 100 pairs in the case the synchronization results in 10 different notes), as given by the quoted formula (that is $8.4 \times 8.6 \times \text{Log} 6 + 8.4 \times 7.0 \times \text{Log} 3 + 8.4 \times 20.8 \times \text{Log} 8 + 8.4 \times 21.7 \times 2 \times \text{Log} 9 + 8.4 \times 18.2 \times \text{Log} 2 + 8.4 \times 2.0 \times \text{Log} 32 + \dots$, sum of 100 terms), is minimal (among different neighbouring choices of synchronization values) for the ratios of frequencies in ascending order (starting from Gly = 1):
1, 6/5, 3/2, 8/5, 9/5, 2, 32/15, 9/4, 12/5, 8/3
giving the following frequencies (from Gly = 220 Hz on):
220, 264, 330, 352, 396, 440, 469.33, 495, 528, 586.67 Hz
corresponding to the notes
low A, C, E, F, G, A, B flat, B, high C, high D
i. e. to within the approximation of the chromatic tempered scale
(i.e. $220 \times$ times an integer power of $2^{1/12}$):
220, 262, 330, 349, 392, 440, 466, 494, 523, 587 Hz
or in the inhibition case:
262, 294, 311, 330, 349, 392, 440, 466, 587, 698 Hz
corresponding to the notes
C, D, E flat, E, F, G, B flat, high D, high F
as claimed.

In cells where the proportions of transfer RNAs (and hence of amino acids) differ from the average, the frequencies may differ slightly from the frequencies on the first line above, but to within the approximation of the chromatic tempered scale, the result has remained unchanged in the some 1000 genes so far transposed according to the method of the present invention. An elementary probabilistic computation (knowing there are about 100 000 genes in the genome) enables one to deduce that the same result must be true for at least 99% of the genes, therefore it has been termed 'universal' (however, exceptions for the last 1% are not excluded).

- % dans les positions		-8.4	8.6	7.0	20.8	21.7	18.2	2.6	8.3	1.3	
n° cadenas (h=01)		4	4	6	14	13	7	2	8	1	
h \ d	d	G	A	S	PV TC	LI ND	QK EM	H	F	RY	W
		0	1	2	3	4	5	6	7	8	9
G - Gly	0	0	1	2	3	4	5	6	7	8	9
A - Ala	1	Log 6	0	1	2	3	4	5	6	7	8
S - Ser	2	Log 3	Log 5	0	1	2	3	4	5	6	7
P-Phe V-Val T-Thr C-Cys	3	Log 8	Log 4	Log 16	0	1	2	3	4	5	6
L-Leu I-Ile N-Asn D-Asp (B-Asx)	4	Log 9	Log 3	Log 6	Log 9	0	1	2	3	4	5
Q-Gln K-Lys E-Glu H-His (Z-GLX)	5	Log 2	Log 5	Log 4	Log 5	Log 10	0	1	2	3	4
H - His	6	Log 32	Log 16	Log 64	Log 4	Log 32	Log 16	0	1	2	3
	[6] [54] [24]		[10] [7]	[36] [7]	[27] [21]	[6] [7]	[27] [24]				
F - Phe [SeC]	7	Log 9	Log 15	Log 3	Log 45	Log 5	Log 9	Log 135 [25] [15]	0	1	2
R - Arg Y - Tyr	8	Log 12	Log 2	Log 8	Log 3	Log 4	Log 6	Log 9 [17] [8]	Log 16	0	1
W - Trp	9	Log 8 [27]	Log 20 [9]	Log 16 [9]	Log 5 [27]	Log 40 [3]	Log 4 [27]	Log 5 [5] [15]	Log 32 [6]	Log 10 [9]	0

Homme
E. G. li

Distances mélodiques (d) et harmoniques (h) entre peptides (acides aminés)

$\langle d \rangle = 3,30 \pm 2,380476$ Avec multiplicité: $2,525 \pm 1,979441145$
 $\langle h \rangle = \pm 1,717498089 \pm 0,9954023322$ [b: 1,732061204]
 $\sigma_d / \sigma_h = 1,352834391$

$\delta = \left(\overline{d} + \left(\frac{\sigma_d}{\sigma_h} \right)^2 \overline{h} \right) / \left(1 + \left(\frac{\sigma_d}{\sigma_h} \right)^2 \right)$
 $\overline{d} = d / \langle d \rangle, \overline{h} = h / \langle h \rangle$

$\mu = 100(1 - \delta)$ niveau musical

θ	1	2	3	4	5	6	7	8	9
α_0	α_1	α_2	α_3	α_4	α_5	α_6	α_7	α_8	α_9
1	$\frac{6}{5}$	$\frac{3}{2}$	$\frac{8}{5}$	$\frac{9}{5}$	2	$\frac{32}{15}$	$\frac{9}{4}$	$\frac{12}{5}$	$\frac{8}{3}$
5	1	$\frac{5}{4}$	$\frac{4}{3}$	$\frac{3}{2}$	$\frac{5}{3}$	$\frac{16}{9}$	$\frac{15}{8}$	2	$\frac{20}{9}$
3	$\frac{5}{4}$	1	$\frac{16}{15}$	$\frac{6}{5}$	$\frac{4}{3}$	$\frac{64}{15}$	$\frac{3}{2}$	$\frac{8}{5}$	$\frac{16}{9}$
2	$\frac{4}{3}$	$\frac{16}{15}$	1	$\frac{9}{8}$	$\frac{5}{4}$	$\frac{4}{3}$	$\frac{45}{32}$	$\frac{3}{2}$	$\frac{5}{3}$
9	$\frac{5}{4}$	$\frac{6}{5}$	$\frac{9}{8}$	1	$\frac{10}{9}$	$\frac{32}{14}$	$\frac{5}{4}$	$\frac{4}{3}$	$\frac{10}{9}$
2	$\frac{5}{3}$	$\frac{4}{3}$	$\frac{5}{4}$	$\frac{10}{9}$	1	$\frac{16}{15}$	$\frac{9}{4}$	$\frac{6}{5}$	$\frac{5}{3}$
3	$\frac{16}{9}$	$\frac{6}{5}$	$\frac{4}{3}$	$\frac{22}{15}$	$\frac{16}{15}$	1	$\frac{135}{128}$	$\frac{9}{8}$	$\frac{5}{4}$
9	$\frac{15}{8}$	$\frac{3}{2}$	$\frac{5}{4}$	$\frac{5}{4}$	$\frac{9}{8}$	$\frac{128}{125}$	1	$\frac{16}{15}$	$\frac{32}{25}$
12	2	$\frac{8}{5}$	$\frac{3}{2}$	$\frac{5}{4}$	$\frac{6}{5}$	$\frac{9}{8}$	$\frac{16}{15}$	1	$\frac{10}{9}$
8	$\frac{20}{9}$	$\frac{16}{9}$	$\frac{5}{3}$	$\frac{40}{27}$	$\frac{4}{3}$	$\frac{5}{4}$	$\frac{32}{27}$	$\frac{10}{9}$	1

Res. de l'eqn
(Cavendish 1914)

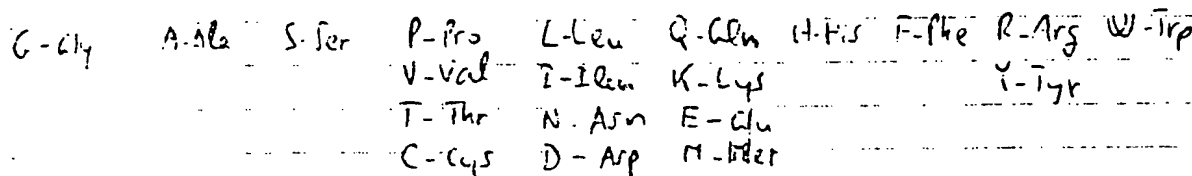
1,80875
(1,77409)
1,66651
(1,48206) -
1,87682 -
(1,73478)
1,79460
(1,46830)
1,97378 -
(1,73119)
1,57488
(1,46132)
2,67338
(1,73478)
2,47608
(1,73478)
1,68066
(1,48183) -
2,19101 -
(1,73478)

$\langle h \rangle = 1,97165$

over lo
multiplicite
 $\langle h \rangle = 1,706$

CALCUL DE LA DISTANCE HARMONIQUE GLOBALE

15482
13113
164
175
157
225
241
262
275



$\left[\begin{array}{cc} \text{Lysine} & \text{IAR} \\ \text{Arginine} & \text{TCN} \end{array} \right] \text{Phe.}$

лсд. 2 112

